

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:19:59 ; Search time 4955.25 Seconds
(without alignments)
11622.905 Million cell updates/sec

Title: US-09-625-573-3

Perfect score: 1979

Sequence: 1 CAGGACTGCGTGAGACAAGC.....ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.ov.*

22: em.pat.*

23: em.ph.*

24: em.pl.*

25: em.ro.*

26: em.sts.*

27: em.un.*

28: em.vi.*

29: em.htg_hum.*

30: em.htg_inv.*

31: em.htg_other.*

32: em.htg_mus.*

33: em.htg_pin.*

34: em.htg_rod.*

35: em.htg_mam.*

36: em.htg_vrt.*

37: em.sy.*

38: em.htgo_hum.*

39: em.htgo_mus.*

40: em.htgo_other.*

41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1979	100.0	1979	6	AR116075	AR116075 Sequence
2	1979	100.0	1979	6	I79543	I79543 Sequence 3
3	1979	100.0	1979	9	HSU03905	U03905 Human monoc
4	1943.8	98.2	5471	9	HS MCPA02	U0924 Human monoc
5	1943.8	98.2	143068	9	HSU35952	AX335952 Sequence
6	1943.8	98.2	143068	9	HSU95626	U95626 Homo sapien
7	1942.2	98.1	185437	9	AC098613	AC098613 Homo sapi
8	1702	86.0	2900	2	AC087602	AC087602 Pan trogl
9	1313	66.3	10528	6	AX345236	AX345236 Sequence
10	1286.4	65.0	10528	6	AX345237	AX345237 Sequence
11	1231.4	62.2	1651	9	HS MCP1REC	X93583 H.sapiens m
12	1083	54.7	1083	6	AX232508	AX232508 Sequence
13	1081.4	54.6	1083	6	AX232506	AX232506 Sequence
14	1081.4	54.6	1083	6	HUM MCP1R	D29984 Human mRNA
15	1079.8	54.6	1083	6	AX280849	AX280849 Sequence
16	1078.2	54.5	1083	6	E13909	E13909 cDNA encodi
17	1023.8	51.7	1083	6	AF013958	AF013958 Macaca mu
18	980	49.5	2232	6	AR116074	AR116074 Sequence
19	980	49.5	2232	6	I79542	I79542 Sequence 1
20	980	49.5	2232	9	HSU03882	U03882 Human monoc
21	780.6	39.4	1364	10	MMU51717	U51717 Mus musculu
22	777.4	39.3	2992	10	MMU56819	U56819 Mus musculu
23	775.8	39.2	1245	10	MMU47035	U47035 Mus musculu
24	769.8	38.9	1365	10	RNU77349	U77349 Rattus norv
25	712.6	36.0	1075	9	AF019379	AF019379 Cercopithec
26	711.8	36.0	1086	9	CAU83324	U83324 Cercopithec
27	711.8	36.0	1086	9	CAU83325	U83325 Cercopithec
28	711	35.9	1059	9	AF035222	AF035222 Cercopithec
29	711	35.9	1059	9	AF081577	AF081577 Cercopithec
30	710.2	35.9	1130	9	AF291669	AF291669 Macaca fa
31	709.4	35.8	1059	9	AF075448	U77672 Macaca mula
32	708	35.8	1966	9	MMU77672	AF075448 Pygathrix
33	707.8	35.8	1059	9	AF005660	AF005660 Macaca fa
34	707.8	35.8	1059	9	AF035217	AF035217 Cercopithec
35	707.8	35.8	1059	9	AF075444	AF075444 Pygathrix
36	707.8	35.8	1059	9	AF141641	AF141641 Cercopithec
37	707.8	35.8	1059	9	AF212101	AF212101 Cercopithec
38	707.8	35.8	1059	9	AF349682	AF349682 Cercopithec
39	706.6	35.7	1059	9	AF075443	AF075443 Trachypit
40	706.6	35.7	1059	9	AF075445	AF075445 Pygathrix
41	706.6	35.7	1059	9	AF177890	AF177890 Macaca ni
42	706.6	35.7	1059	9	AF177892	AF177892 Trachypit
43	706.6	35.7	1059	9	AF005662	AF005662 Macaca mu
44	706.2	35.7	1059	9	AF035223	AF035223 Cercopithec
45	706.2	35.7	1059	9	AF051905	AF051905 Cercopithec

ALIGNMENTS

RESULT 1	1979 bp	DNA	Linear	PAT 16-MAY-2001
AR116075	AR116075	Sequence 3 from patent US 6132987.		
LOCUS	AR116075	Sequence 3 from patent US 6132987.		
DEFINITION	AR116075	Sequence 3 from patent US 6132987.		
ACCESSION	AR116075	Sequence 3 from patent US 6132987.		
VERSION	AR116075.1	GI:14096397		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1979)			
AUTHORS	Charo, I.F. and Coughlin, S.R.			
TITLE	Recombinant mammalian monocytic chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)			
JOURNAL	Patent: US 6132987-A 3 17-OCT-2000;			

Query Match									
Best Local Similarity 100.0%; Score 1979; DB 6; Length 1979;									
Matches 1979; Conservative 0; Mismatches 0; Indels 0; Gaps									
QY	1	CAGGACTGCCTGAGACAAGCCACACAGCTTGAACAGAGAAAGTGATTTGAACAAGGACGCAT	60						
DB	1	CAGGACTGCCTGAGACAAGCCACACAGCTTGAACAGAGAAAGTGATTTGAACAAGGACGCAT	60						
QY	61	TTCCCCAGTAGATCCACAACATGCTGTCCACATCTCGTTCTCGGTTTATTCAGAAATACCA	120						
DB	61	TTCCCCAGTAGATCCACAACATGCTGTCCACATCTCGTTCTCGGTTTATTCAGAAATACCA	120						
QY	121	ACGAGAGCGGTGAAGAAGTACCAACCTTTTTTGATTATGATTACGGTGCCTCCTGTGCATA	180						
DB	121	ACGAGAGCGGTGAAGAAGTACCAACCTTTTTTGATTATGATTACGGTGCCTCCTGTGCATA	180						
QY	181	AAATTGACGTGAAGCAAAATTGGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGGTGTCA	240						
DB	181	AAATTGACGTGAAGCAAAATTGGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGGTGTCA	240						
QY	241	TCTTTGGTTTGTGGGCAACATGCTGTGTCCTCACTTAACTGCAAAAAGCTGA	300						
DB	241	TCTTTGGTTTGTGGGCAACATGCTGTGTCCTCACTTAACTGCAAAAAGCTGA	300						
QY	301	ASGTGCTTGACTGACATTTACCTGTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTTA	360						
DB	301	ASGTGCTTGACTGACATTTACCTGTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTTA	360						
QY	361	CTCTCCCATTTGGGGTCACTCTGCTCAAAATGAGTGGCTTTTGGGAATGCAATGTGCA	420						
DB	361	CTCTCCCATTTGGGGTCACTCTGCTCAAAATGAGTGGCTTTTGGGAATGCAATGTGCA	420						
QY	421	AATTATTTCAGGGCTGTATCACATCGGTTATTTTGGCGGAATCTCTTCATCATCTCTCC	480						
DB	421	AATTATTTCAGGGCTGTATCACATCGGTTATTTTGGCGGAATCTCTTCATCATCTCTCC	480						
QY	481	TGCAATCGATAGATACCTTGGCTATTGTCCATGCTGTGTTTGTCTTTAAAAAGCCAGGACGG	540						
DB	481	TGCAATCGATAGATACCTTGGCTATTGTCCATGCTGTGTTTGTCTTTAAAAAGCCAGGACGG	540						
QY	541	TCACCTTTGGGTGGTGACAAGTGATCACCTGGTGTGGTGGCTGTGTTTGCCTCTCTCC	600						
DB	541	TCACCTTTGGGTGGTGACAAGTGATCACCTGGTGTGGTGGCTGTGTTTGCCTCTCTCC	600						
QY	601	CAGGAATCATCTTTACTAAATGCCAGAAAGAGATCTGTTTATGTCTGTGGCCCTTATT	660						
DB	601	CAGGAATCATCTTTACTAAATGCCAGAAAGAGATCTGTTTATGTCTGTGGCCCTTATT	660						
QY	661	TTCACAGGAGATGGAATATTTCCACACAATATGAGGAACATTTTGGGCTGGTCTCTGC	720						
DB	661	TTCACAGGAGATGGAATATTTCCACACAATATGAGGAACATTTTGGGCTGGTCTCTGC	720						
QY	721	CGTGCTCATCATGTCTACTCTCGGGAATCCTGAAAACCCCTGCTTCGGTGTCTGAA	780						
DB	721	CGTGCTCATCATGTCTACTCTCGGGAATCCTGAAAACCCCTGCTTCGGTGTCTGAA	780						
QY	781	ACGAGAAAGAGGATAGGGCAGTGAGATCATCTTCACCATCATGATTGTTTACTTTC	840						
DB	781	ACGAGAAAGAGGATAGGGCAGTGAGATCATCTTCACCATCATGATTGTTTACTTTC	840						
QY	841	TCCTCTGGACTCCCTATTAACATTTGCAATCTCCTGAAACACCTTCCAGGAATTTCTCGGCC	900						
DB	841	TCCTCTGGACTCCCTATTAACATTTGCAATCTCCTGAAACACCTTCCAGGAATTTCTCGGCC	900						
QY	901	TGAGTAACTGTGAAGCACCAGTCAACTGGACCCAGCCACGAGTGACAGACTCTTTG	960						
DB	901	TGAGTAACTGTGAAGCACCAGTCAACTGGACCCAGCCACGAGTGACAGACTCTTTG	960						

DEFINITION Sequence 3 from patent US 5707815.
ACCESSION I79543
VERSION I79543.1 GI:3207833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1979)
AUTHORS Charo, I.F. and Coughlin, S.R.
TITLE Mammalian monocyte chemoattractant protein receptors and assays
using them
JOURNAL Patent: US 5707815-A 3 13-JAN-1998;
FEATURES Location/Qualifiers
 1..1979
 /organism="unknown"
BASE COUNT 530 a 435 c 451 g 563 t
ORIGIN

Query Match 100.0%; Score 1979; DB 6; Length 1979;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACTGCTGAGCAAGCCACAAAGCTGAACAGAGAAAGTGGATTGAACAGAGCGCAT 60
DB 1 CAGGACTGCTGAGCAAGCCACAAAGCTGAACAGAGAAAGTGGATTGAACAGAGCGCAT 60
QY 61 TTCCCCAGTACATCCACAAATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCA 120
DB 61 TTCCCCAGTACATCCACAAATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCA 120
QY 121 ACAGAGCGGTGAAGAGTCAACACCTTTTGGATTATGATTACGCTGCTCCCTGCATTA 180
DB 121 ACAGAGCGGTGAAGAGTCAACACCTTTTGGATTATGATTACGCTGCTCCCTGCATTA 180
QY 181 AATTTCAGTGAAGCAAAATGGGGCCCACTCCTCGCTCGCTCTACTCGCTGGTGTCTCA 240
DB 181 AATTTCAGTGAAGCAAAATGGGGCCCACTCCTCGCTCGCTCTACTCGCTGGTGTCTCA 240
QY 241 TCCTTGGTTTGGGCAACATGCTGGTCTCTCACTCTGATCTCTGTTTCTTTATTA 360
DB 241 TCCTTGGTTTGGGCAACATGCTGGTCTCTCACTCTGATCTCTGTTTCTTTATTA 360
QY 301 AGTGTCTGACTGACATTTACTCTCAACTGCACTGCTCTGATCTCTGTTTCTTTATTA 360
DB 301 AGTGTCTGACTGACATTTACTCTCAACTGCACTGCTCTGATCTCTGTTTCTTTATTA 360
QY 361 CTCTCCCATTTGGGCTCACTCTGCTGCAATAGTGGGTCTTTGGGAATGCAATGTGCA 420
DB 361 CTCTCCCATTTGGGCTCACTCTGCTGCAATAGTGGGTCTTTGGGAATGCAATGTGCA 420
QY 421 AATTATTCAGGGCTGTATCAGATCGGTTATTTTGGGGAATCTTCTTCATCATCTCC 480
DB 421 AATTATTCAGGGCTGTATCAGATCGGTTATTTTGGGGAATCTTCTTCATCATCTCC 480
QY 481 TGCAATCGATAGATACCTGCTATTGTCATGCTGTTTGGCTTTAAAGCCAGGAGCG 540
DB 481 TGCAATCGATAGATACCTGCTATTGTCATGCTGTTTGGCTTTAAAGCCAGGAGCG 540
QY 541 TCACCTTTGGGGTGGTGACAAAGTGTGATACCTGGTGGTGGCTGTGTTGCTCTGTCC 600
DB 541 TCACCTTTGGGGTGGTGACAAAGTGTGATACCTGGTGGTGGCTGTGTTGCTCTGTCC 600
QY 601 CAGGAATCATCTTTACTAAATGCCAGAAAGAGATCTGTTTATGCTGTGCGCTTATT 660
DB 601 CAGGAATCATCTTTACTAAATGCCAGAAAGAGATCTGTTTATGCTGTGCGCTTATT 660
QY 661 TTCACAGAGGATGAATTAATTTCCACACAATAATGAGGAACATTTTGGGGCTGGTCTGC 720
DB 661 TTCACAGAGGATGAATTAATTTCCACACAATAATGAGGAACATTTTGGGGCTGGTCTGC 720
QY 721 CGCTGCTCATCATGCTGATCTGCTACTCGGGAATCCTGAAACCCCTGCTCGGTTCCGAA 780
DB 721 CGCTGCTCATCATGCTGATCTGCTACTCGGGAATCCTGAAACCCCTGCTCGGTTCCGAA 780

781 ACGAGAAGAAGAGGATAGGGCAGTGGAGTCACTTCCACCATCATGATGTTTACTTTC 840
DB 781 ACGAGAAGAAGAGGATAGGGCAGTGGAGTCACTTCCACCATCATGATGTTTACTTTC 840
QY 841 TCCTCTGGACTCCCTATAACATTTGTCATTTCTCTGTAACACCTTCCAGGAATTTCTGGGC 900
DB 841 TCCTCTGGACTCCCTATAACATTTGTCATTTCTCTGTAACACCTTCCAGGAATTTCTGGGC 900
QY 901 TGAGTAACCTGTGAAGAGCAGTCACTGAGCAAGCCAGCGAGGTGACAGACACTCTTG 960
DB 901 TGAGTAACCTGTGAAGAGCAGTCACTGAGCAAGCCAGCGAGGTGACAGACACTCTTG 960
QY 961 GGATGACTCACTGCTGATCAATCCCATCATCTATGCTTCTGTTGGGAGAACTTCAGAA 1020
DB 961 GGATGACTCACTGCTGATCAATCCCATCATCTATGCTTCTGTTGGGAGAACTTCAGAA 1020
QY 1021 GGTATCTCTCGGTGTTTCTCCGAAAGCAGATCAACCAAGCGCTTCTGCAACAATGTCAG 1080
DB 1021 GGTATCTCTCGGTGTTTCTCCGAAAGCAGATCAACCAAGCGCTTCTGCAACAATGTCAG 1080
QY 1081 TTTTCTACAGGAGAGACAGTGGATGGAGTCAACAAACACGCGCTTCCACTGGGAGC 1140
DB 1081 TTTTCTACAGGAGAGACAGTGGATGGAGTCAACAAACACGCGCTTCCACTGGGAGC 1140
QY 1141 AGGAAGTCTCGGTGTTTATAAAACGAGGAGCAGTTTGAATGTTTATAAAGGAGGA 1200
DB 1141 AGGAAGTCTCGGTGTTTATAAAACGAGGAGCAGTTTGAATGTTTATAAAGGAGGA 1200
QY 1201 TAAACAATCTGTATATAACAACAACCTTCAAGGGTTTGTGAACAAATAGAAACCTGTAAAG 1260
DB 1201 TAAACAATCTGTATATAACAACAACCTTCAAGGGTTTGTGAACAAATAGAAACCTGTAAAG 1260
QY 1261 CAGGTGCCCAGGAGACCTCAGGCTGTGTACTAATACAGACTATGTACCCCAATGTCATA 1320
DB 1261 CAGGTGCCCAGGAGACCTCAGGCTGTGTACTAATACAGACTATGTACCCCAATGTCATA 1320
QY 1321 TCCAAATGCTGCTCAGGGAATAATCCAGAAAAAAGTGGGTGAGAGACTTTCAGTCTCCAG 1380
DB 1321 TCCAAATGCTGCTCAGGGAATAATCCAGAAAAAAGTGGGTGAGAGACTTTCAGTCTCCAG 1380
QY 1381 AAAGCTCATCTCAGCTCCTGAAATGCTTCAATACCTTGTGCTTAATCTCTTTTCTAG 1440
DB 1381 AAAGCTCATCTCAGCTCCTGAAATGCTTCAATACCTTGTGCTTAATCTCTTTTCTAG 1440
QY 1441 TCCTCAATATTTCTTCACTCAATCTCTGATCTGTCATGCTTGAATCAAGGCCAGC 1500
DB 1441 TCCTCAATATTTCTTCACTCAATCTCTGATCTGTCATGCTTGAATCAAGGCCAGC 1500
QY 1501 TGGAGGTGAAGAAGAGATGTGACAGGCACAGATGAATGGGAGTGAGGATAGTGGGTC 1560
DB 1501 TGGAGGTGAAGAAGAGATGTGACAGGCACAGATGAATGGGAGTGAGGATAGTGGGTC 1560
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DB 1561 AGGCTGAGAGAGAGAGGAGAGATGAGCATGGCTGAGCTGAGCAAAAGACAAAGGT 1620
QY 1621 GAGCAAAAGGCTCAGCAGATTTCAGCCAGGAGATGATGCTGCTTAGCCCCATCTGCCAC 1680
DB 1621 GAGCAAAAGGCTCAGCAGATTTCAGCCAGGAGATGATGCTGCTTAGCCCCATCTGCCAC 1680
QY 1681 GTGTATTTAACTTGAAGGTTTCAACAGGTGAGGAGAGTTGGGAACCTGCAATACCTG 1740
DB 1681 GTGTATTTAACTTGAAGGTTTCAACAGGTGAGGAGAGTTGGGAACCTGCAATACCTG 1740
QY 1741 GGAGTTTGGTGGAGTCCGATGATTTCTTTTGCATTAAGTGCATGACATATTTTCTGCTTT 1800
DB 1741 GGAGTTTGGTGGAGTCCGATGATTTCTTTTGCATTAAGTGCATGACATATTTTCTGCTTT 1800
QY 1801 ATTACAGTTTATCTATGCGACCCATGCACTTACATTTGAAATCTATGAAATATCATGCT 1860
DB 1801 ATTACAGTTTATCTATGCGACCCATGCACTTACATTTGAAATCTATGAAATATCATGCT 1860

QY	327	AACCTGGCCATCTCTGATCTCTGCTTTTCTTTCTTTATTA	CTCTCCCATTTGGGCTCACTCTGCT	386
DB	1852	AACCTGGCCATCTCTGATCTCTGCTTTTCTTTATTA	CTCTCCCATTTGGGCTCACTCTGCT	1911
QY	387	GCAATGAGTGGGCTTTTGGGAATGCAATGTGCAAAATTA	TTTCACAGGGCTGTATCACATC	446
DB	1912	GCAATGAGTGGGCTTTTGGGAATGCAATGTGCAAAATTA	TTTCACAGGGCTGTATCACATC	1971
QY	447	GGTTATTTTGGCGGAATCTTCTTCATCATCCTCTCTGACA	ATCGATAGATACCTTGGCTATT	506
DB	1972	GGTTATTTTGGCGGAATCTTCTTCATCATCCTCTCTGACA	ATCGATAGATACCTTGGCTATT	2031
QY	507	GTCCATCTGTGTTTGGCTTTTAAAGCCAGACGGTCACTTT	GGGGTGTGACAAAGTGTG	566
DB	2032	GTCCATCTGTGTTTGGCTTTTAAAGCCAGACGGTCACTTT	GGGGTGTGACAAAGTGTG	2091
QY	567	ATCACCTGGTGTGGCTGTGTTTGTCTCTCCAGGAATCATCT	TTACTAATGCCAG	626
DB	2092	ATCACCTGGTGTGGCTGTGTTTGTCTCTCCAGGAATCATCT	TTACTAATGCCAG	2151
QY	627	AAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACG	AGGATGGAATAATTTCCAC	686
DB	2152	AAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACG	AGGATGGAATAATTTCCAC	2211
QY	687	ACAATATGAGGAACATTTTGGGCTGTGCTCCCGCTGCTCA	TGTCATCTGCTAC	746
DB	2212	ACAATATGAGGAACATTTTGGGCTGTGCTCCCGCTGCTCA	TGTCATCTGCTAC	2271
QY	747	TCGGGAATCCTGAAACCCCTGCTTCGGTGTGCAAGAGAGG	CATAGGGCAGTG	806
DB	2272	TCGGGAATCCTGAAACCCCTGCTTCGGTGTGCAAGAGAGG	CATAGGGCAGTG	2331
QY	807	AGAGTCATCTTACCATCATGATTGTTTACTTCTCTTGAC	TCCCTTACATGTTCTGCTAC	866
DB	2332	AGAGTCATCTTACCATCATGATTGTTTACTTCTCTTGAC	TCCCTTACATGTTCTGCTAC	2391
QY	867	ATTCTCCTGAACACCTTCAGGAATTTTCGGCCTGAGTAAC	TGTGAAAGCACCAGTCAA	926
DB	2392	ATTCTCCTGAACACCTTCAGGAATTTTCGGCCTGAGTAAC	TGTGAAAGCACCAGTCAA	2451
QY	927	CTGGACCAAGCCAGCGAGTGACAGAGCTCTTGGGATGAC	TCACTGCTGATCAATCCC	986
DB	2452	CTGGACCAAGCCAGCGAGTGACAGAGCTCTTGGGATGAC	TCACTGCTGATCAATCCC	2511
QY	987	ATCATCTATGCCCTCGTTGGGAGAGTTTCAAGAGTATCTC	TGCGTGTCTTCCGAAAG	1046
DB	2512	ATCATCTATGCCCTCGTTGGGAGAGTTTCAAGAGTATCTC	TGCGTGTCTTCCGAAAG	2571
QY	1047	CACATCACCAGCGCTTCTGCAACAATGTCAGTTTTTCTAC	AGGGAGACAGTGGATGGA	1106
DB	2572	CACATCACCAGCGCTTCTGCAACAATGTCAGTTTTTCTAC	AGGGAGACAGTGGATGGA	2631
QY	1107	GTGACTTCAACAAACACGCCCTTCCACTGGGAGCAGGAAG	TCTCGGCTGTTTATAAATC	1166
DB	2632	GTGACTTCAACAAACACGCCCTTCCACTGGGAGCAGGAAG	TCTCGGCTGTTTATAAATC	2691
QY	1167	GAGGAGCAGTTTGATTTGTTTATAAGGAGATATAACAAT	TCTGATATAACAACAACT	1226
DB	2692	GAGGAGCAGTTTGATTTGTTTATAAGGAGATATAACAAT	TCTGATATAACAACAACT	2751
QY	1227	TCAAGGGTTTGTGAACAATAGAACCCTGTAAGCAGGTGCC	AGGACCTCAGGCTGT	1286
DB	2752	TCAAGGGTTTGTGAACAATAGAACCCTGTAAGCAGGTGCC	AGGACCTCAGGCTGT	2811
QY	1287	GTGTACTAATACAGCTATGTACCCCAATGCATATCAACAT	GTGCTCAGGGAATAATCC	1346
DB	2812	GTGTACTAATACAGCTATGTACCCCAATGCATATCAACAT	GTGCTCAGGGAATAATCC	2871
QY	1347	AGAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCA	TCTCAGCTCCTGAAAAAT	1406
DB	2872	AGAAAACTGTGGGTAGAGACTTTGACTCTCCAGAAAGCTCA	TCTCAGCTCCTGAAAAAT	2931
QY	1407	GCCTCAATACCTTGGCTAAFCCTCTTTTCTAGCTTCTCA	TATAATTTCTTCACCTCAATCTC	1466

Db	2932	GCCTCATTA	CTGTGCTAAT	CTCTTTTCTAGTCTT	CAATAATTC	TTCTTCACTCA	ATCTC	2991
QY	1467	TGATTCGT	CAATGCTCTT	TGAATCAAGGGCC	AGCTGGAGGTGAAGAGAA	TGTGCACG	1526	
Db	2992	TGATTCGT	CAATGCTCTT	TGAATCAAGGGCC	AGCTGGAGGTGAAGAGAA	TGTGCACG	3051	
QY	1527	GCACAGAT	GAATGGGAGT	GAGGATAGTGGGGT	CAGGCTGAGAGGAA	GAGGAGAC	1586	
Db	3052	GCACAGAT	GAATGGGAGT	GAGGATAGTGGGGT	CAGGCTGAGAGGAA	GAGGAGAC	3111	
QY	1587	ATGAGCAT	GGCTGAGCCT	TGCACAAAGCTGAGCAAA	GGGCTCAGCGATTCAGCC	A	1646	
Db	3112	ATGAGCAT	GGCTGAGCCT	TGCACAAAGCTGAGCAAA	GGGCTCAGCGATTCAGCC	A	3171	
QY	1647	GGAGATGAT	ACTGGTCTT	AGCCCATCTGCCACGTG	TATTAACCTTGAAGGGTTCACC		1706	
Db	3172	GGAGATGAT	ACTGGTCTT	AGCCCATCTGCCACGTG	TATTAACCTTGAAGGGTTCACC		3231	
QY	1707	AGGTCAGG	GAGATTTGGGA	ACTGCAATACCTGGGAGT	TTTGGTGGAGTCGCGATGATTC		1766	
Db	3232	AGGTCAGG	GAGATTTGGGA	ACTGCAATACCTGGGAGT	TTTGGTGGAGTCGCGATGATTC		3291	
QY	1767	TCCTTTGC	ATAAGTGCATGACAT	ATTTTGGCTTATACAGT	TTTATCTATGCGACCCATG		1826	
Db	3292	TCCTTTGC	ATAAGTGCATGACAT	ATTTTGGCTTATACAGT	TTTATCTATGCGACCCATG		3351	
QY	1827	CACCTTAC	ATTGAAATCTATGA	ATATCATGCTCCATTTGGT	TCAGATGCTTCTTAGGCCA		1886	
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QY	1887	CATCCCCCT	GTCTAAAAATTCAGAAA	ATTTTGGTTTATAAAA	AGATGCTATATCTATGATA		1946	
Db	3412	CATCCCCCT	GTCTAAAAATTCAGAAA	ATTTTGGTTTATAAAA	AGATGCTATATCTATGATA		3471	
QY	1947	TGCTAATAT	ATGCTATATGCAAT	ATAATAA			1973	
Db	3472	TGCTAATAT	ATGCTATATGCAAT	ATAATAA			3498	

RESULT	5
LOCUS	AX335952
DEFINITION	Homo sapiens
ACCESSION	Sequence 6461 from Patent WO0194629.
VERSION	AX335952.1 GI:18126671
KEYWORDS	.
SOURCE	human.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
REFERENCE	Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z. Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL	Patent: WO 0194629-A 6461 13-DEC-2001;
FEATURES	Avalon Pharmaceuticals (US) . Location/Oualifiers 1..143068 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	41194 a 30122 c 32403 g 39349 t
ORIGIN	

		98.2%;	Score	1943.8;	DB	6:	Length	143068;		
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Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Giacalone,J., Pae,A., Powell,E., Solinsky,K.A., Desilva,U., Diaz-Perez,S., Zhou,X., Yu,Y., Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.
Human BAC clone 110P12
Unpublished (1997)

TITLE JOURNAL REFERENCE AUTHORS

McCombie,R.W., Wilson,R., Chen,E., Gibbs,R., Zuo,L., Johnson,D., Nhan,M., Parnell,B., Dedhia,N., Ansari,A., Mardis,E., Schuttz,K., Ghoj,L., de la Bastide,M., Kaplan,N., Greco,T., Touchman,J., Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Giacalone,J., Pae,A., Powell,E., Solinsky,K.A., Desilva,U., Diaz-Perez,S., Zhou,X., Yu,Y., Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.
Direct Submission

TITLE JOURNAL

Submitted (27-MAR-1997) Advanced Genome Analysis Course,
Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor,
NY 11724, USA

COMMENT

Regions with single-strand coverage are as follows:

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FEATURES source

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 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
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 and Haugen, E.D.
 Direct Submission
 Unpublished
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 Box 352145, Seattle, WA 98195, USA
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 Direct Submission
 Submitted (01-AUG-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 On Aug 1, 2002 this sequence version replaced gi:16445164.

 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgchgs@u.washington.edu

 Project Information
 Center project name: chr-3
 Center clone name: RP11-24F11 (bc0137)

 Summary Statistics
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator ET; 93% of reads
 Assembly: Dye-terminator Big Dye; 7% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 184860 bases at least Q40
 Consensus quality: 185398 bases at least Q30
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 Insert size: 185437; sum-of-contigs
 Quality coverage: 7.6x in Q20 bases; sum-of-contigs

 Overlapping Sequences:
 5': BAC-110P12 U95626, 111014-bp overlap
 3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
 all regions were either double-stranded or sequenced with an
 alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing
 problems, such as compressions and repeats; all regions were
 covered by at least one plasmid subclone or more than one M13
 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
 fingerprinting. Comparison of the experimentally derived digest
 fragments with sequence-predicted fragments is given below.
 The electronically-digested sequence consists of both insert and
 vector, in order to accurately represent the entire circular BAC.
 Small fragments below a variable cutoff (approximately 400-800 bp)
 are not resolved in the fingerprint and hence do not appear
 in the table. There are no significant remaining discrepancies
 between the experimental and predicted values. Uniquely ordered
 fragments are separated by dashed lines.

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RESULT 8
AC087602/c
LOCUS
DEFINITION Pan troglodytes clone RP43-177M18, *** SEQUENCING IN PROGRESS ***,
1 unordered piece.
ACCESSION AC087602
VERSION AC087602.3 GI:14190646
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Pan troglodytes
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 2900)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

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Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R.,
 Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
 Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H.,
 Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
 Earhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M.,
 Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
 Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E.,
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
 Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
 Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.,
 Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseg, H.,
 Lozano, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
 Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M.,
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, S.,
 Nguyen, N., Nickerson, E., Nwokoko, S., Ogih, M., Okwuonu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, T.,
 Rives, M., Rojas, A., Rojokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
 Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.

TITLE

JOURNAL

Unpublished

2 (bases 1 to 2900)

Worley, K. C.

Direct Submission

Submitted (14-JAN-2001)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 2900)

Worley, K. C.

Direct Submission

Submitted (08-MAR-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 23, 2001 this sequence version replaced gi:12621388.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: ZUAC

Center clone name: RP43-177M18

----- Summary Statistics

Sequencing vector: M13; L08821

Chemistry: Dye-primer Body: 61% of reads

Chemistry: Dye-terminator Big Dye: 38% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 15117 bases at least Q40

Consensus quality: 28463 bases at least Q30

Consensus quality: 43561 bases at least Q20

Estimated insert size: 21502; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank-draft-data.html>)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES	source	Location/Qualifiers
BASE COUNT	808 a 656 c 633 g 803 t	
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Query Match	86.0%;	Score 1702; DB 2; Length 2900;
Best Local Similarity	96.8%;	Pred. No. 0;
Matches 1768; Conservative	0; Mismatches	55; Indels 3; Gaps
QY	151 TTGATTATGATTCAGGTGCCCTGTCATTAATTTGACGTGAAGCAAAATTTGGGCGCCAAAC	210
DB	2609 TCGAATTTATATACATATCGAGGCCCTGCCAAAATAATCATGTGAGCAAAATTCGACGCCGCC	2550
QY	211 TCCCTGCCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTGTGGGCAACAATGCTGTCG	270
DB	2549 TCCCTGCCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACAATGCTGTCG	2490
QY	271 TCCCTCATCTTAAATAACGTGAAAAGCTGAAGTGGTTCGACTGCATTTACCTGCTCAACC	330
DB	2489 TCCCTCATCTGATAAATCTGCAAAAGGCTGAAGAGCATGACATGATATCTACTGCTCAACC	2430
QY	331 TGGCCATCTCGATCTGCTCTTTCTTATTACTTCCCAATGTGGGCTCAGCTCTGCTGCAA	390
DB	2429 TGGCCATCTCGACCTGTCTTTCTCTCTTACTCTCCCAATGTGGGCTCAGCTCTGCTGCAA	2370
QY	391 ATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTAATCACAGGCGTGTATCACATCGGTT	450
DB	2369 ATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTAATCACAGGCGTGTATCACATCGGTT	2310
QY	451 ATTTTGGGGGAATCTTTTCATCATCTCTGACAAATCGATAGATACCTGGCTATTGTCC	510
DB	2309 ATTTTGGGGGAATCTTTTCATCATCTCTGACAAATCGATAGATACCTGGCTATTGTCC	2250
QY	511 ATGCTGTGTTTCTTTTAAAGCCAGAGCGGTCAACCTTTGGGGTGGTGACAAGTGTGATCA	570
DB	2249 ATGCTGTGTTTCTTTTAAAGCCAGAGCGGTCAACCTTTGGGGTGGTGACAAGTGTGATCA	2190
QY	571 CCTGGTGGTGGCTGTGTTTGTCTGTGCCAGGAATCATCTTTACTAAATGCCAGAAG	630
DB	2189 CCTGGTGGTGGCTGTGTTTGTCTGTGCCAGGAATCATCTTTACTAAATGCCAGAAG	2130
QY	631 AGAATCTGTTTATGCTCTGCGCCCTATTTTCCAGGAGTGAATAATTTCCACACAA	690
DB	2129 AGAATCTGTTTATGCTCTGCGCCCTATTTTCCAGGAGTGAATAATTTTCCACACAA	2070
QY	691 TAATGAGGAACATTTTGGGGCTGGTCTCGCGCTGCTCATATGTCATCTGCTACTCGG	750
DB	2069 TAATGAGGAACATTTTGGGGCTGGTCTCGCGCTGCTCATATGTCATCTGCTACTCGG	2010
QY	751 GAATCTGAAAACCCCTGCTTCGGGTGTCGAAACAGAGAAGAGGCATAGGGCAGTCAGAG	810
DB	2009 GAATCTGAAAACCCCTGCTTCGGGTGTCGAAACAGAGAAGAGGCATAGGGCAGTCAGAG	1950
QY	811 TCATCTTCACCATCATGATTTTACTTCTCTCTGGAATCCCTATAACATTTGCTATTC	870
DB	1949 TCATCTTCACCATCATGATTTTACTTCTCTCTGGAATCCCTATAACATTTGCTATTC	1890
QY	871 TCTGTGAACACTTCCAGGAATTTCTGGGCTGAGTAACCTGAAAGCACAGTCAACTGG	930
DB	1889 TCTGTGAACACTTCCAGGAATTTCTGGGCTGAGTAACCTGAAAGCACAGTCAACTGG	1830
QY	931 ACCAAGCCAGCGAGGTGACAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCA	990

[illegible]

RESULT 9

AX345236	AX345236	10528 bp	DNA	linear	PAT 01-FEB
LOCUS	Sequence 307 from Patent WO0200928.				
DEFINITION	Sequence 307 from Patent WO0200928.				
ACCESSION	AX345236				
VERSION	AX345236.1	GI:18493122			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	synthetic construct.				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Olek, A., Piepenbrock, C. and Berlin, K.				
TITLE	Diagnosis of diseases associated with the immune system				
JOURNAL	Patent: WO 0200928-A 307 03-JAN-2002;				
	Epigenomics AG (DE)				
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source	1..10528				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="chemically treated genomic DNA (Homo sapiens)"				
BASE COUNT	3072 a 86 c 2419 g 4951 t				
ORIGIN					
	Query Match 66.3%; Score 1313; DB 6; Length 10528;				
	Best Local Similarity 79.7%; Pred. No. 0;				
	Matches 1550; Conservative 0; Mismatches 395; Indels 0; Gaps				
QY	29 GAACAGAGAAGTGGATTGAACAGGACGACATTTCCCCAGTACATCCACACATGCTGTC	88			
Db	8327 GAATAGAGAAGTGGATTGAATAGGACGATTATTTTAGTATATATATATATGTTGTT	8386			
QY	89 CACATCTCGTTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTCCACACCTT	148			
Db	8387 TATATTTTCGTTTCGGTTTATTAGAAATATTAACGAGAGCGGTGAAGAAGTATTATTT	8446			
QY	149 TTTTGATTATGATACGGTCTCCCTGCTATAAATTGACGTGAAGCAAAATTGGGGCCCA	208			
Db	8447 TTTTGATTATGATACGGTCTCCCTGCTATAAATTGACGTGAAGTGAAGTGAAGTGAAG	8506			
QY	209 ACTCTCGCTCCGCTCTACTCGCTGGTGTTCATCTTTGTTTGTGGGCAACATGCTGGT	268			
Db	8507 ATTTTGTGTTTCGTTTATTCGTTGCTGTTATTTTGGTTTGGGTAATATGTTGGT	8566			
QY	269 CGTCTCATCTTAATAAATGCAAAAGCTGAAGTGGTGTGACTGACATTTACCTGCTCAA	328			
Db	8567 CGTTTATTTTAATAAATGTAAGAAGTGAAGTGTGATGATGATTTATTTGTTTAA	8626			
QY	329 CCTGCCATCTCTGATCTGCTTTTCTTATATCTCTCCCATGTGGGTCACCTCTGCTGC	388			
Db	8627 TTTGGTTATTTTGAITTCGTTTTTTTATATATTTTATTTGTTGGGTTATTTGTTGT	8686			
QY	389 AAATCAGTGGGCTTTTGGAAATGCAATGTGCAAAATTTTCACAGGGCTGTATCACAATCG	448			
Db	8687 AAATCAGTGGGCTTTTGGAAATGCAATGTGCAAAATTTTCACAGGGCTGTATCACAATCG	8746			
QY	449 TTATTTTGGCGGAATCTTCTTCATCATCTCTCCCTGACATCGATAGACTGCTGCTATGCT	508			
Db	8747 TTATTTTGGCGGAATCTTCTTCATCATCTCTCCCTGACATCGATAGACTGCTGCTATGCT	8806			
QY	509 CCATCTGTGTTTGGCTTTAAAGCCAGACGGTCACTTTTGGGTTGGTGACAAAGTGTGAT	568			
Db	8807 TTATGTTGTTGTTTGTGTTTAAAGTTAGACGGTTATTTTGGGTTGGTGATAGTGTGAT	8866			
QY	569 CACCTGGTGTGGCTGTGTTGCTCTCTCCAGGAATCATCTTTACTAAATGCCAGAA	628			
Db	8867 TATTGGTGTGGTGTGTTGTTTGTGTTTATAGGAATATATTTTATTAATGTTAGAA	8926			
QY	629 AGAAGATCTGTTATGTCGTGGCCCTTATTTTCCAGGAGATGGAATAATTTCCACAC	688			
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QY	689 AATAATGAGGAACATTTTGGGCTGGTCTCCGCTGCTCATCATGCTGCTACTGCTACTC	748			
Db	8987 AATAATGAGGAATATTTTGGGTTGGTCTGCTGTTTATATGTTATTTGTTATTC	9046			

1641 CAGCCAGGAGATGATCTGGTCTCTAGCCCATCTGCCACGCTGATTTAAACCTTGAAGGG 1700
 DB CAGCCAGGAGATGATCTGGTCTCTAGCCCATCTGCCACGCTGATTTAAACCTTGAAGGG 960
 1701 TTCACAGGTCAGGAGAGTCTGGGAAGTGCATTAACCTGGAGGTTTGGTGGAGTCCGA 1760
 DB TTCACAGGTCAGGAGAGTCTGGGAAGTGCATTAACCTGGAGGTTTGGTGGAGTCCGA 1020
 1761 TGATCTCTTTGGCATAGTGCATGACATATTTTGGCTTTATACAGTTTATCTATGGCA 1820
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 1821 CCCATGACCTTACATTTGAAATCTATGAATATATCATGCTCCATGTTTCAGATGCTTCT 1880
 DB CCCATGACCTTACATTTGAAATCTATGAATATATCATGCTCCATGTTTCAGATGCTTCT 1140
 1881 AGCCACATCCCGCTCTCAAAAATTCAGAAAATTTTCTTATATAAGATGCAATATCT 1940
 DB AGCCACATCCCGCTCTCAAAAATTCAGAAAATTTTCTTATATAAGATGCAATATCT 1200
 1941 ATGATATGCTATATATATATATATATATATATATAA 1973
 DB ATGATATGCTATATATATATATATATATATATAA 1233

RESULT 12
 AX232508 1083 bp DNA linear PAT 11-SEP-2001
 LOCUS Sequence 3 from Patent WO0162796.
 DEFINITION AX232508
 ACCESSION AX232508.1 GI:15592570
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1083)
 Valdes A.M., Groot P.H. and Spurr N.K.
 Ccr2-641, polymorphic variant of the human ccr2 receptor and its
 use in the diagnostic and treatment of atherosclerosis
 Patent: WO 0162796-A 3 30-AUG-2001;
 JOURNAL SMITHKLINE BEECHAM PLC (GB)
 FEATURES
 Location/Qualifiers
 source
 i. 1083
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 255 a 260 c 247 g 321 t
 ORIGIN

Query Match 54.78; Score 1083; DB 6; Length 1083;
 Best Local Similarity 100.0%; Pred. NO. 6.2e-287;
 Matches 1083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

81 ATGCTGTCACATCTCGTCTCGGTTATCAGAAATACCAAGAGAGCGGTGAAGAGTC 140
 DB 1 ATGCTGTCACATCTCGTCTCGGTTATCAGAAATACCAAGAGAGCGGTGAAGAGTC 60
 141 ACCACCTTTTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 200
 DB 61 ACCACCTTTTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 201 GGGGCCCAACTCCCTCCGCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260
 DB 121 GGGGCCCAACTCCCTCCGCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 261 ATGCTGGTGGTCTCTATCTTATAAAGTGCATTAAGTGCATTAAGTGCATTAAGTGCATTAAGT 320
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 321 CTGCTCAACCTGGCCATCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
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 681 TTCCACACAATATAGGAAACATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
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 DB AGTCAACTGGACCAAGCCAGCTGACAGAGACTCTTGGGATGACTCACTGCTGCTGCTGCTGCT 900
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 DB AATCCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGAGTATCTCTCGGTGCTGCTGCTGCT 960
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 DB CGAAAGACATCACCAAGCGCTTCTGCAAAACAATGTCAGTTTCTACAGGAGACAGTG 1020
 1101 GATGAGTGAATTTCAACAAACACCGCTTCCACTGGGAGAGAGTCTCGGCTGCTGCTGCT 1160
 DB GATGAGTGAATTTCAACAAACACCGCTTCCACTGGGAGAGAGTCTCGGCTGCTGCTGCTGCT 1080
 1161 TAA 1163
 DB 1081 TAA 1083

RESULT 13
 AX232506 1083 bp DNA linear PAT 11-SEP-2001
 LOCUS Sequence 1 from Patent WO0162796.
 DEFINITION AX232506
 ACCESSION AX232506
 VERSION AX232506.1 GI:15592569
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1083)
 Valdes A.M., Groot P.H. and Spurr N.K.
 Ccr2-641, polymorphic variant of the human ccr2 receptor and its
 use in the diagnostic and treatment of atherosclerosis

QY 621 TGCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
Db |
QY 541 TGCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 600
Db |
QY 681 TTCACACAATAATGAGAAACATTTTGGGGCTGTCTGCCGCTGCTCATCATGGTCAATC 740
Db |
QY 601 TTCACACAATAATGAGAAACATTTTGGGGCTGTCTGCCGCTGCTCATCATGGTCAATC 660
QY 741 TGCTACTCGGGAATCCTGAAAAACCTGCTTCCGGGTGTCGAAACGAGAGAAAGAGCATAGG 800
Db |
QY 661 TGCTACTCGGGAATCCTGAAAAACCTGCTTCCGGGTGTCGAAACGAGAGAGAGCATAGG 720
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QY 721 GCAAGAGAGTCAATCTTCCACCATCATGATTGTTTACTTTCTTCTTGGACTCCCTATAAC 780
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QY 781 ATGTCTCATCTCTGAAACACCTTCCAGGAATCTTCCGGGTGTCGAAACGAGAGAAAGAGCATAGG 840
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QY 981 AATCCCATCATCTATGCTTCTGTTGGGGAGAGTTTCCAGAGGATCTCTCGGTGTTCTTC 1040
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QY 1021 GATGAGTCACTTCAACAAACAGCGCTTCCACTGGGGAGCAGGAAGTCTCGGTGTTTA 1080
QY 1161 TAA 1163
Db |
QY 1081 TAA 1083

Search completed: June 1, 2003, 18:46:52
Job time : 5316.25 secs